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OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
pred. No. is the number of results predicted by chance to have a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      May 3, 2003, 23:04:17; Search time 5082.23 Seconds (without alignments) 17041.707 Million cell updates/sec
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2: gb_htg:
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gb_htg:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFE AU T1	RESULT 1 KFBGLUG LOCUS DEFINITIO ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANI		42 C 43 45	39 40 41	C 37	C 34 35		c 29 30		25		c 20	17 18	c 15	12 13	c 10	0 80 ~		ωN	1	Result
REFERENCE AUTHORS TITLE	TION ION ION DS		2 104.4 3 104.4 4 104.4 5 104.4	111.	11/ 114 111	123	127.6 126.4	29.	200	78		152.2	776	178.2	197.4 184.4 184.4	. 7		 393.6	406.2 393.6	427	core
Saccharomyces frag	KFBGLUC Kluyveromyces fra X05918 GI:2804 X05918.1 GI:2804 beta-glucosidase- beta-glucosidase- Kluyveromyces mar Kluyveromyces mar Kluyveromyces mar		3 3 3 0 5 5 5 5	, w w w		4.1 4.0	4.2	207 262	4.6 2166 4.5 3158			010	5.4 2230 5.3 2640 5.3 3179	.9 12441	.2 3241 .2 17665	9.1 110000 $6.9 2601$ $6.6 37445$	3710		305	4193	% Query Match Length DB
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s,M.C. and Guerineau,M. beta-glucosidase gene of Saccharomyces cerevisiae	ν γ γ γ γ γ γ γ γ γ γ γ γ γ γ γ γ γ γ γ		AC023491 Homo sap- AJ414153 Yersinia	evote ostri yersi		AE004598 Pseudomon			집	092808 Ruminococcu AR205082 Sequence		AE005849 Cauloback AE012240 Xanthomon	74.0		Y14327 Saccharopol		Continuation (3 of	32973	P.)	581 9 Sc	cripti

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BASE COUNT 1338 a
                                                                                      Query Match 14.3
Best Local Similarity 50.7
Matches 1253; Conservative
339 ATGGCTGATATTGATGTTGAAGGCCATCTTGAAGAAGGTCACCCTGGCCGAGAAGGTCGAT 398
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/note="inverted repeat A'"

8 675 c 941 g 1239 t
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FKTEFGRVVYGEDIFVGYRYYEKLQRKVAFPFGYGLSYTTFELDISDFKVTDDKIDIS
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                                                                                                                                                                                                                                                                                                                                                                      /note="yeast termination consensus sequence"
3498. .3501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AISYFNEELGKWHVEAGEYLVSVGTSSDDILSVKEFKVEKDLYWKGL"
                                                        14.3%; Score 427; DB 8; Length 4193; 50.7%; Pred. No. 1.1e-46; rative 0; Mismatches 1155; Indels 63; Gaps
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/db_xref="GI:2805"
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/codon_start=1
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/strain="ATCC 12424"
/db_xref="taxon:4911"
/clone_lib="PHCG3"
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-GGAGAACGGCCCCAGAGAAACGGCCACAGAAACGGCACACAGAGACAAGAAG	GCGCA: ACGTTI AC	GCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTTATGGTTCTGGTTTGTTCTACTTAAACGATGAGTTGATTATTGACCAAAAGCACAAC 2111
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                                                                                                                                                                                                                                                                                                                                                          CTAGTTCAAGCTTGGTACGGTGGTAATGAATTGGGTAATGCTATCGCAGATGTCTTGTAC 2582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCATCTGCGCGGGCCTTAACGCCGACTGGGAGACCGAGGGCGCGACCGCGAGCATG
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CTATCGTATACAACATTCGAACTAGATATTTCTGACTTCAAGGTAACTGATGATAAGATA 2822
                                        CTGTCCTACACCACTTTTGCCTTTTCCAATCTCTCCGTGTCTCACAAGGACGGCAAGCTG
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                                                                                          GTTGGTTATAGGTACTACGAAAAGCTTCAAAGAAAGGTAGCCTTCCCCTTCGGATATGGT
                                                                                                                                  GTCGGGTACAGGTACTACGAGTTTGCCGACAAGGACGTCAATTTCCCCCTTTGGCCACGGC 2444
                                                                                                                                                                               CCAGCCTTTTTAAACTTCAAGACCGAGTTCGGAAGAGTTGTTTACGGTGAGGATATCTTT 2702
                                                                                                                                                                                                                          CCCGCGTTTCTCAACTTCCGCACCGAGGCCGGGCGCACGCTGTACGGCGAGGACGTCTAC
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32244 TCGAGGAACTGGTCGACCGGATGACGCTCGAGGAGCAGGTGAGCCTGTTATCGGGCGAGG 32303
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                                         GATGCAATTTCCTACTTTAACGAAGAGCTCGGTAAATGGCACGTTGAAGCAGGTGAATAC 3062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Uncultured bacterium aminoglycoside 3'-N-acetyltransferase gene,
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1 (bases 1 to 38269)
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August, P.R. and Martinez, A.
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IVEAFLATGRGKRGEVGEASSVLVPAAAMVAFGVDWLERWGKTL"
12117 c 12998 g 6835 t 1 others
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RTTPGALRSGSPGASMAALGGEAEWFTADHALDYGYGPQSPLGKLVEAEGKVLMLGAP
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/codon_start=1
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                                                                                                                                                                                                                                                                                                     /product="aminoglycoside 3'-N-acetyltransferase"
/protein_id="AAL92107.1"
/db_xref="GI:19569566"
/translation="WTSRVAFRSSLADDLSAIGLADGDAVLVHAALRQVGKIVGGPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="uncultured bacterium"
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	1491 33359	1432 TCAGCAAGCAGCTCGAGACGCCGCCATCGTACACCGTCGGCGGCTACACCACCGTTCCTC	₽ ₹
	1431 33320	1372 ACCACGGCGGAGGCTCTGCCGCACTCAGGGCCTACTACGCAGTCACTCCCTTTGACGGCCC	₽ 24
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	1191 33083	1132 TTATCCACGTCATTGACCAGAGGGCTAGGGAAGTTCTTCAGTTCGTCAAGAAGTGTGCTG	₽ &
	113 <u>1</u> 33023	1072 CCGGACCTCCACGCTTCCGAGGAGAAACACTCAAGTTCAACGTCTCCAACGGGAAAGCCCT 	ρ δ
	1071 32963	1012 ACTGGTACGGCACATACAGTACCACAGAAGCCGTTGTGGCAGGCCTCGACCTCGAGATGC	₽ 2
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	951 32843	892 AGCCGGGTGCGTTCATGACGGCGTACAATGGCATCAATGGCGTGTGCTGCAGCGAGAACC	gb Qy
	891 32783	832 CGGAGCGGGCTCTCCGTGAAATCTACGCACTCCCGTTCCAGATTGCTGTGCGAGACTC	g 8
	831 32723	772 TCAAGCACTTTTTGTGCAATGATCAGGAGGACAGGCGCATGATGGTGCAGAGCATCGTCA	B S
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	; 711 , 32603	7 652 TGCAACGCTCCCCTCTCGGTGGACGTGGCTTCGAGTCGATTGGTGAGGATCCGTTCCTGG	무양
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CACAGGTGGCCCAGCTCTACGTCAAGCCCCTCCAAGCGGCCAAGATTAACCGCCCCCGTCA 2607	Þ	Qy
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2 CCGGCGTGCTGGACCAGCTCATTGCCGACGTGGCCGCCGCGGAACCCCAAACACCGTCGTCG 2151	2092 CC 11 33936 CC	Qy Db
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GATCCGTTCCTGGCGGGCTTGGGAGCTGCGGCTCTCATCCGCGGCATTCAGAGCACTGGA 758
                               CCAACGGTAAATATCCATCGTGGACCCTTAAATGGTAGGGGTTTTGAATCATTTTCTGAA
                                                   CCGACTATCAACATGCAACGCTCCCCTCTCGGTGGACGTGGACTTCGAGTCGATTGGTGAG
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                                                                                                GAAGTTGGTGAATATTTAGCAGAAGAAGCAAAAGCGAAAGGTGTTAGTGTGTTTTGGGT
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Direct Submission
Submitted (02-AUG-1995) W. Richard McCombie, Cold
Submitted (02-AUG-1995) W. Richard McCombie, Cold
Spring Hart
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                                                                                                                                                               AAGGATGGCTATTTCTATATAGACATTGAAGGTTATTTAATTCCTGACGACGACGCTGTT
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                                                                               TATGAATTTGGGATATCTGTGTTTGGAACGGCTCTGCTGTTATTGATGATGTCTTATTA
                                                                                                                       GACGATTACGATTTAGAAGATGGAGTTGTTCGTTTTTACGATTATTGTAACGACAAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGAGAAATTCTATTTAATTTAAAGAAGGGGAGAAAGTATAATGTACGGGTCGAGTATGGA 10053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGACGGGCCGCATCAATCTCGTCAAGGGCAACACGTACAAGTTCAAGATCGAGTTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTAGCAAACATTATTTTTGGAGAGCAAAACCCTTGTGGAAAATTGCCAATAACATTCCCT 10473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAATCCAATCCCAATACAGTAGTTGTGACTCAATCAGGCACTCCAATTGAGATGCCATGG
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                                                                                                                                                                   TCTGAAGAGGGCGAGTACAACGTTCTTGTCGGAACCAGCAGTAAAG 10936
                                                                                                                                                                                                                                                                                                                                                                                          GCAGAAATTATACAAGTATATTTCTCAAATC---GTTCGTTCAGTTAATCGACCTGTT 10770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTGTGGTGAAAGGTTAAGGATCGATTTGGAGATTTCGAATACTGGCCCCCATGTCTGGT 10713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCCCCTTTGGCCACGGCCTGTCCTACACCACTTTTGCCTTTTCCAATCTCTCCCGTGTCT 2486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAAACTGAAGGATAATCCTGCCTATCTTTCATTTCGTTCAAGCCGTGGCCATTGTGTT 10533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTGCCGACGTCGTCTTTGGCGACTACAACCCCTCGGGCAAGCTGTCCCTCAGCTTCCCC 2306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCTCTGAAGCCCACACCTTATTGCACATTTGGTACAACGGTAACGAATTAGGAAATGCT 10413
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                                                                                                                                                                                                      GTCGAAAAGGGTGACTATGAGGTTATCGTGAGCGACAGCAGCGCAG
                                                                                                                                                                                                                                                                              ATCGAGGAGCAGGAGAAGTACGTCGCTGCGTATTTTGATGAGGAGCGGGATCAGTGGTGT 2726
                                                                                                                                                                                                                                                                                                                                                       AAGGAGCTCAAGGGCTTCGCAAAGGTCGAACTGCAGCCCGGCGAGACGAAGGCGGTGACA 2666
                                                                                                                                                                                                                                                                                                                                                                                                                               GCACAGGTGGCCCAGCTCTACGTCAAGCCCCTCCAAGCCGCCCAAGATTAACCGCCCCGTC 2606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTCCATTTGGATATGGGCTTTCATATACTACTTTTGAATTATCCAATCTTTATTTGAAG 10653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATGGAGAAGACGTCTTTGTTGGGTATAAGTATTATGAAGCCGTAGAAAGGGAGGTCTTG 10593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGCGCCTGCAGGACAACCCCGCGTTTCTCAACTTCCGCACCGAGGCCGGGCGCACGCTG
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                                                                                                                                                                                                                                             ATTGAGTTGGATATAAAGTATGCTACTTCTTTTTATGATGAACTTAATGAAAAATGGTGT 10890
                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe cosmids AL355920
adenosine deaminase; alpha-glucosidase; beta-glucosidase
                   AL355920.1
                                                                       SPBC1683
                   GI:7801293
                                                                       41799 bp
                                                        c1683.
   precursor
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         small overlap between neighbouring submissions. Cosmid SPBC1683 is overlapped at its 5' end by cosmid SPBC359 and at its 3' end by cosmid SPBC1198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP
pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (11-APR-2000) W. Richard McCombie, Cold Spring Harbor Lab, 1 Bungtown Rd, P.O. Box 100, Cold Spring Harbor, NY 11754, USA and Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The length in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McCombie, W.R. and Lyne, M.H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Details of yeast sequencing at the Sanger Centre are available the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overlapping sections once, or longer, because we arrange for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Notes:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fission yeast.
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SIIGYGNVMWIFCGCMWGGILFTLLLPETKGRDADEIDRVELFYGGDGKVECNSKWKS
                                          AIGNLIIAVAGYVPGYWENVFLVEILGRKWIQLQGFVITGLMFAILAGRWNEISTGGR
FACFVIAQLFSNFGPNSTTFIYPAEVFPARVRGTAHGISAALGKCGAILASLLFNFLT
                                                                                                                                   TSLNFEDDELVKNPSVTKGHPEIHESSENYLSRSNTVENEPENIEKQFESVSAPANRS
GFIQYFROMHHFKHLLGTSVCWFLLDIAFYGVNLNQSVILKNIGFSSGTNEYRTLMKN
                                                                                                                                                                                                                                       RWLLGYGIGGDYPMSAAITSERSKLNRRGTLISLIFAFQGFGTLAGAIVTIILLGCFE
HPLNREGHYRKLEGVWRLQFGLALVPAIGVLIPRLMMEETQKFKNSQQLNSGDNRDPK
                                                                                                                                                                                                                                                                                                                                      /translation="mklnifkshgdsntaeerpvpleqveaedqohenrfwlgltake
frlmmlagvgffldsydlfinlvtpifeylywggiekgpngkghypsgirglvnaas
nignifgqlmggfmgdffgrkvygkemiiviiatilliampksihsplskmmwvfcw
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB91163.1"
/db_xref="GI:7801294"
/translation="Temporary for the protein of the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY:Schizosaccharomyces pombe, YAEC_SCHPO, pu inorganic phosphate transporter c23d3.12., (559 aa), scores: opt: 2395, E():0, (70.0% identity in 574 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="cosmids 359 (partial), 1198 and 1683"
/clone_lib="Mizukami, et al., 1993. Cell 73:121-132."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Schizosaccharomyces pombe"
/db_xref="taxon:4896"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="mRNA from spc08587 1 193"
3226. .4947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="nominal overlap with cosmid SPBC359
phromosome II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="IIL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SPBC1683.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="SPBC1683.01, len:573,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 4947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPBC1683.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7448. .9007)
/gene="SpBC1683.03c"
/gene="SpBC1683.03c, len:519, SIMILARITY:Saccharomyces
/note="SpBC1683.03c, len:519, SIMILARITY:Saccharomyces
cerevisiae, Q08902, orf yor378w., (515 aa), fasta scores:
opt: 2052, E():0, (58.0% identity in 509 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASAYD".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="partial degraded TF1-type LTR" 5967. .6986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVFVETACTAQLMTQAGLGQSIAPNNIIGKSLGTTNPGQLSWFPASYSLTVGTFILIA
GRLGDIYGHKKMFVLGYIWFCIWSLISGFSYYAKSVIMFDVCRALTGIAPAFLLPNAL
ALLGRYYPPGKKKNLIFALFGATAPNGFLLGSVFSGIFAQLSWNPWTYNTTAIVCIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              deaminase Score 164.32"
complement(7448. .9007)
/gene="SPBC1683.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEEIKESYNFHDLASFLEVYYEGVELLLHEODFYDLCYQYLRKAASONVYYABMFTDD
QLHTRRGISFBTVIKGLIRARDDAMRDFHIYSOLIMC FIREMSFENAEETLNASLPYK
SEIIGIGLDSMEENNPPIKFIKVFQRAROLCYREUTCHCDLHOKNTTTHIROALEDIGV
ERIDHGINILDDPELIKLALERNIPFTVCPFSNEIVYPGKAQPEIRIMLDTGLKVTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transporter Score 132.7 complement(5308. .5478)
                                                                                                                                                                                       /product="beta-glucosidase
glycosyl hydrolase family 3
/protein_id="CAB91166.1"
/db_xref="GI:7801297"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDDPAYMHCFYITENFNLAQKGASLTKKELVQICRNSFEAAWISEEKRNHYLEALNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative adenosine deaminase"
/protein_id="CAB91164.1"
/db_xref="G1:7801295"
/translation="MTDIERFIEKLPKAELHLHLEGTLEAELKLKLSHRNKIPLKQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Match to PF00083 sugar_tr,
transporter Score 132.74"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(3364.
                          SIDVSQRALREVYLMPFQLACKYSNFKSLMTSYNKVNGEHVSQSRILLDNILRKEWEW
KGTIISDWFGTYSLKKAIDAGLDLEMPGKPRFRNVNTIQHLVGSKELSESILDERAKN
VLKLVKHSWQNTEAENHCELNNDSSCLREALKKFASQSIVLLKNKKKLLPLSRKGTFA
                                                                                                                                      /translation="mmehdvedLINQLDISEKAMLLSGTDLWHTAAIPRLNIPSIRLS
DGPNGIRGTSFFNSSPSACFPCGTALGATFDKKLLFEVGEYLAEEAKAKGVSVVLGPT
                                                                                                                                                                                                                                                                                                                                                                                                                     marxianus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SPBC1683.04"
11335. .13833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIGELSLYVFYLVEKRYVQPILAPSMMNSEMGCYLICYAAGWACFGIWMYYLWQFLEN
LRFATPLLVTAQLTPYGISGCAAALTTGYLLKRLKPTKIMYVSMIAFTYGTILIATAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIIGYFAIPHIEADEVEEKQKFDYLGAFFGVSGLVLINFSWNQGPVVGWQVPYVYILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="MFS transporter of unkown specificity"
/protein_id="CAB91165.1"
/db_xref="GI:7801296"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Match to PF00962 A_deaminase, Adenosine/AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SPBC1683.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /labe1=SPBC1683.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SPBC1683.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SPBC1683.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(3364. .4004,4134. .4872)
/gene="SPBC1683.01"
                                                                                                           VNIHRGPLNGRGFESFSEDSTLSGLAASYVILGLQSKNVQACIKHFVCNDMEDERNSV
                                                                                                                                                                                                                                                                                                                                                                848 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SPBC1683.04" len:832, SIMILARITY:Kluyveromyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPLIMKNTKAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=SPBC1683.03c
VIGPNAKVCNYSGGGSANLKPYYTVSMYDGIAAKIDGVPEYALGCHNYLNLPNIANLL
                                                                                                                                                                                                                                                                                                         /label=SPBC1683.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IHQTYWAQTFVSIIVTPWGMDMSFPAATLMLSDFVPKQHQGIAASLVSTVVNYSISIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MMNYVKSLGTYNTRNMEKESSKDLVQNEDTPLPVQKISMSLFHE"
                                                                                                                                                                                                                                                                                                                                   codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                        anus, BGLS_KLUMA, beta-glucosidase precursor, (845 fasta scores: opt: 1274, E():0, (46.3% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 13833
                                                                                                                                                                                                                                                    precursor (EC
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                                                                                                                                                                                                                                                                         3.2.1.21);
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Best Local Similarity Matches 1199; Conserv
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Best Local :
                                                                                                                                                                                                                                                                                                                                                         11575 GAAGTTGGTGAATATTTAGCAGAAGAAGCAAAAGCGAAAGGTGTTAGTCTGGTTTTGGGT 11634
                                                                                                                       11515 TCCGCTTGTTTTCCCTGTGGGACAGCGCTAGGGGCTACTTTCGACAAAAAGTTACTATTC 11574
                                                                                                                                                                                                                                        11455 ATTAGATTATCAGACGGCCCTAATGGTATCCGTGGAACTAGCTTCTTCAATTCTTCACCA 11514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11335 ATGATGGAACATGATGTTGAAGATTTGATCAATCAATTGGATATAAGTGAGAAGGCTATG 11394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
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                                                              579
                                                                                                                                                                            519 GCGGCCTGCCTTGCGGCACGTCGCTCGGTTCCACATTCAACCAAACTCTGCTCGAA 578
                                                                                                                                                                                                                                                                                             459 CTCCGCTTTACAGATGGCCCCAACGGCGTAAGAGGGGACCAAGTTCTTCAATGGCGTCCCT 518
                                                                                                                                                                                                                                                                                                                                                                                                                     399 CTGCTGGCTGGTATCGACTTCTGGCACACAAAGGCTCTCCCCAAGCATGGAGTCCCCTCT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 ATGGCTGATATTGATGTTGAGGCCATCTTGAAGAAGCTCACCCTGGCCGAGAAAGGTCGAT 398
                                                           GAGGCAGGTAAGATGATGGGCAAAGAGGCCATCGCTAAGAGTGCGCATGTGATCCTCGGC 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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LAALIAGNVFIAMPMTLNGLEGSHYHLPFAVOSRASFGYFFRTLIILLRFIAGLFYYG
TNVYTGAECVOTILYAIFKSERSYKNRLPADAGITSDFLISYEYYMVISFPFHILIPE
YLORFFLIKSISTYIAGFAMLIFLCLNGGSHVVWDQPATVSGRSWSWVFMCALNSSVA
GFSTLAVNVNDETRYVKHPKTPYVOMLILPLVAAVSAPIGIUSGVASKIMYGTAMWDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="SPBC1683.05, len:559, SIMILARITY:Saccharomyces cerevisiae, THIY_YEAST, putative thiamine transporter yor192c., (599 aa), fasta scores: opt: 828, E():0, (26 identity in 512 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIIQVYISQIVRSVNRPVKELKEFSKVVLCPKETKLIRIELDIKYATSFYDELNEKWC
SEEGEYNVLVGTSSKDIALTGKFTLPKTIHWTGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LCVGLTAEWETEGEDRKTMTLPSLSDKLVYSILQSNPNTVVVTQSGTPIEMPWISEAH
TLLHIWYNGNELGNALANIIFGEQNPCGKLPITFPKKLKDNPAYLSFRSSRGHCVYGE
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GRKYNVRVEYGSAATYTLSTNLSPSTGGRYSIGCVKVIDPETEIDYAVRVAKSVDCVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNPRTGKHGYVAKFYLEPATSENRTLIDDYDLEDGVVRFYDYCNDKMKDGYFYIDIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SPBC1683.06c" | Ien:310, SIMILARITY:Escherichia /note="SPBC1683.06c, len:310, SIMILARITY:Escherichia coli., YBEK_ECOLI, hypothetical 33.8 kd protein in leus-gitl intergenic region., (311 aa), fasta scores: opt:838, E():0, (44.5% identity in 308 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="NCS1 allantoate transporter"
/protein_id="CAB91167.1"
/db_xref="GI:7801298"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SPBC1683.05"
17673. .19352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SPBC1683.06c"
complement(20737. .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVIIIGAWAIVPWKILQNGTAFLAFLGSLSIFLGPAAGIFVADKFKNHHKYDIDEFYN
PSGIYRYNKLGLNWRALIAFLCACVPLIPGMAMSINPSITMPDGVIHLYYIGYFYSFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative inosine-uridine preferring nucleoside hydrolase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(20737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAFLIYWGLNLVFPAKETLLEEAVYPPKSNAELVDPSTLSGKDKFWYYIDY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQIANNWTSRGGRAAAFFMGLTYLVSMIAQNISDNTVAÄANDLLYFFPRYLDIRRAQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MEDPKSDEKFDIGISEKNLDVGFGESSSVDVPVKGRFASFLKKL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=SPBC1683.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SPBC1683.05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SPBC1683.04"
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                                           GCGGCAGACACGTGGTACGCCGACATGGAGGGCACGTACACCGCCGACGACGACTGCACC
                                                                                                                                                                                                                                                                                  CATAACTATCTAAACCTTCCAAATATTGCAAATTTATTAGTCAACCCTAGAACCGGCAAG
                                                                                         GACGATTACGATTTAGAAGATGGAGTTGTTCGTTTTTACGATTATTGTAACGACAAAATG
                                                                                                                                     GACGAGCTCTTCACCAAGACGGACATGCACCTGGTGGACTACTACCACCCCAA----G
                                                                                                                                                                                   CATGGATACGTTGCGAAGTTTTATCTTGAACCTGCAACCTCCGAAAATAGAACTTTGATA 12591
                                                                                                                                                                                                                                   CCGGGCATGCGCTGGAGGGTCTTCAACGAGCCCCCTGGTACCCCTAACCGCCAGCACATT
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                                                                 29596 AGTATTGACGTCTCACAAAGGGCACTTAGAGAAGTATATCTTATGCCATTTCAGTTGGCA 2965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTAGATTATCAGACGGCCCTAATGGTATCCGTGGAACTAGCTTCTTCAATTCTTCACCA 2929
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                  GTGCGAGACTCCCAGCCGGGTGCGTTCATGACGGCGTACAATGGCATCAATGGCGTGTCG 938
                                                                                                        CAGAGCATCGTCACGGAGCGGGCTCTCCGTGAAATCTACGCACTCCCGTTCCAGATTGCT
                                                                                                                                                       GTCCAAGCATGCATTAAGCATTTTGTGTGTAATGATATGGAAGATGAAAGGAACTCTGTC 29595
                                                                                                                                                                                                 GTGCAGGCTACGATCAAGCACTTTTTGTGCAATGATCAGGAGGACAGGCGCATGATGGTG 818
                                                                                                                                                                                                                                           GATTCTACTTTATCAGGTCTTGCAGCTAGTTATGTTATTCTTGGATTGCAAAGTAAAAAC 29535
                                                                                                                                                                                                                                                                                       GATCCGTTCCTGGCGGCCTTGGGAGCTGCGGCCTCTCATCCGCGGCATTCAGAGCACTGGA 758
                                                                                                                                                                                                                                                                                                                                   CCAACGGTAAATATCCATCGTGGACCCTTAAATGGTAGGGGTTTTGAATCATTTTCTGAA 29475
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Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-1995) W. Richard McComble, Cold Spring Harbor Lab, 1 Bungtown Rd, P.O. Box 100, Cold Spring Harbor, NY 11754,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCombie, W.R.
Direct Submission
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/clone_lib="Mizukami, et al., 1993. Cell 73:121-132.
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1. .85837
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                                                                                     Molecular cloning, characterization and expression beta-glucosidase gene from the edible straw mushroc
                                                                                                                                                                           Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Agaricales; Pluteaceae; Volvariella.
                                         Unpublished
                                                                     volvacea
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                    GCAGAAGGGTGGAATTGGTGCTACTATCAAACATTTTGTCGGAAACGACAAGGAGGACGA
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LKPEGGAIKKIAVVGGNAKAGVLSGGGSAALKASYFISPYGGIKAALEPHGVEVTFSE
GARAYKTLPTLEWDLETETGERGWIGTWHTHESDDSMTALDQPFIAPRLVDETRIFIS
TSYPKGITKRWIMRIKGYLKPREKDTWREFGLIAAGBAKLWVDGQLVLDNWTRQRRGE
AFFGSGSGEETGYYLLKAGKKHEIYVEYCNVRAPADGDEDEAIMDSNPGVRLGGAEVA
RADDLLSEAVKLASEADAVIAVVGLNADWETEGNDRFULALFGRÜDELVEKVAKVNSK
TVVVTQAGSAITLPWLDSVAAVVHAWYLGANFODAIADVLFGKQNPSGKLSJTFFKRL
EDVPSHGHFGSENGKVRYAEDLFVGYKHYHHRNIEPLFPFGFGLSYTTFSLSNLQLSA
PVIDHATSSFSLTATLSITNTGPVTGSEVAQLYVSYBETSELTHAFAGLARAFKQKKDL
PVIDHATSSFSLTATLSITNTGPVTGSEVAQLYVSYBETSELTHAFAGLARAFKQKKKKDL
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/db_xref="GI:12584217"
/translation="mppsdfakanideivequtldeaisltagvgfwhthaierlgvp/translation="mppsdfakanideivequtldeaisltagvgfwhthaierlgvpAvvvSdgpngirgnhermgtpakclpsstalgatwdpevveevglkkllapeaklraas
avvvSdgpngirgnhermgtpakctprstagaisasyvwgvQkkgigatikheygndke
LVLapysniqrhplggressessesdpylsgiisasyvwgvQkkgigatikheygndke
DDRQGydsiiseralreiyllpfmltqkyaapwaimtaynrvwgvhvaedpfllkQvl
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CACCTACACCCTCAAGGGCGACACCATCGTCCCCGGCCACGGCTCCCTCC	CAATCTCGTCAAGGGCAACACGTACAAGTTCAAGATCGAGTTCGGCTCCGCACC 18	CARGCAGGTCCCCGGCGATGCCTTCTTCGGCTCCGCCGCCGCGAGAAAAAGGGCCCAAAAAAAGGTCGTGAGAAAAAAAA	CGTCGTCTGCGGCAAAGGCGTAGGTAGACGACCAGCTCGTCGTCGACCAACGCCAC 1	CGCCGACATGGAGGGCACGTACACCGCCGACGAGGACTGCACCTACGAGCTCGGCCT 172	CACCAAGACGGACATGCACCTGGTGGACTACTACCACCCCAAGGCGGCAGACACGTGGTA 166	CAACGAGCCCCTGGTACCCCTAACCGCCAGCACATTGACGAGCTCTTCTT 16	CATTCTAGGCGAGCAGTGCCTCACGCCCGACGGCGCTCCGGGCATGCGCTGGAGGGTCTT 155	GACGCCGCCATCGTACACCGTCGGCGCCTACACCACCGTTCCTCC 1492	TGCCGCACTCAGGGCCTACTACGCAGTCACTCCCTTTGACGGCCTCAGCAAGCA	GAAGAAGACGCTGATTGTCGGCCCCAACGCCAAGGCAGGC	GGGCATCGTGCTGAAGAACAACGAGAACAACGTTCTGCCCTTGAGCAAGAA 1327	CGAGACGACTGTCAACAACACCCCCCGAAACGGCAGCTCTCCTCCGGAAGGTTGGCAACGA 1276	AGTTCTTCAGTTCGTCAAGAAGTGTGCTGCCTCCGGAGTGACGGAGAACGGCCC 121	CAAGTTCAACGTCTCCAACGGAAAGCCCTTTATCCACGTCATTGACCAGAGGGCTAGGGA 116	TGTGGCAGGCCTCGACCTCGAGATGCCCGGACCCTCCACGCTTCCGAGGAGAAACACT 110	GGGTTGGGATGGCCTAATCATGAGCGACTGGTACGGCACATACAGTACCACAGAAGCCGT 104	CAATGGCGTGTCGTGCAGCGAGAACCCTAAATATCTTGATGGGATGCTTCGAAAGGAATG 985 	GTTCCAGATTGCTGTGCGAGACTCCCAGCCGGGTGCGTTCATGACGGCGTACAATGCCAT 925
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                                                                                                                                                                                                                                                                                         504 GGCGGGCGCACCGTCGCGCTGTTCCCCCAACGCGACCCTGCTCGCGTCCGCGTGGAGCGAG 563
                                                                                                                                                                                                                                                                                                                           564 GAGTCGACGAGGTCGGCCGGCTGCTCGCCGAGGAGGCCCTCGCGCAGCAGATCCAC
                                                                                                                                                                                                                                                                                                                                                                                             447 GGAGTCCCCTCTCCCCCTTTACAGATGGCCCCAACGGCGTAAGAGGGGACCAAGTTCTTC 506
                                                                                            GTCGTGCTCGGCCCCACGATCAACCTGCACCGCTCCGTGCTCGGCGGACGCCTGTTCGAG
                                                                                                                                       GTGATCCTCGGCCCGACTATCAACATGCAACGCTCCCCTCTCGGTGGACGTGGCTTCGAG 686
                                                                                                                                                                                                                                           ACTCTGCTCGAAGAGGCAGGTAAGATGATGGGCAAAGAGGCCCATCGCTAAGAGTGCGCAT 626
                                           TCGATTGGTGAGGATCCGTTCCTGGCGGCCTTGGGAGCTGCGGCTCTCATCCGCGGCATT 746
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9511746
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Submitted (27-MAY-1997) Biochemistry, The Hong Kong University of Science and Technology, Clear Water Bay Road, Kowloon, Hong Kong Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 11.8%;
Similarity 48.7%;
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//Gb_xref="GI:2921740"
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//translation="MTSGROTALDPAALVASLPLETKVRLLTGATAFTLAPEESIGLGEV
/translation="MTSGROTVALFPNATILASAWSEESTTEVGRLLAEEALAQQIHVVL
GPTINLHRSVLGGRLFEAYSEDPLLTGRLAAAYVRGLQDLGVCACLKHLVANUSETER
RTMNSVVDPATLRELYLLPFEIAVDESDPWSYMAAYNDVNGVPATEHHHVVNEVLKGE
WGYTGLVMSDWFATRTAAPAAAGGLDLVMPGPDGPWGBALVARYSGELDESVVDDHL
RRLLVLAARVCALGDLRDYPDDLAFADSAVREEQLTRLAAAGMTVLTNADDTLFLARG
TRVALVGRHALETIDMGGGSATVNPPYQVSVAEGLTALLGDAVDVVDGVEVRTRPVPA
RPGFVVDPDTGRPGLHTLLAAAGTVLDERHDAPSTYMVGFDDDFPQAVARVRFRARV
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GDLEXTEGRFVGYRGHWADRAPAPAFWLGHGLGYATWEYADATLDTDGDAPAVTVTVT
NTGARTSREVVGVYLEPASSDEPVRLYGWADATVDAGASARVTVTADARMWRRWDEAA
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DATVVLRSSTRSVTVCDADFGTDAGAAAEPLAGVGLFGLVARPAPEAEDDVITRAAAA
DADVAVVVGGTEEEETESVDKSTIALFGAQDALVEAVAAAARRTVVVVNAATFVL
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/note="one type of cellulase"
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QY 1815 GCCACCGGGAGGAGACGGGCCGCATCAATCTCGTCAAGGGCCAACACGTACAAGTTC 1871	Ö
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Qy 1755 GACCAGCTCGTCGACAACGCCACCAAGCAGGTCCCCGGCGATGCCTTCTTCGGCTCC 1814	ø
Db 1704 GCGATCGGCGTCGGACGGTGGCAGGTGACCGCAGGGGGCACCGAGGCTCGCCTGGACGCTC 1763	D
CCTCGTCGTCTGCGGC	Ø
Db 1644 GCGTCGCCGCGTCCGGTTCCGTGCCGGCGTCGCCGAGGTCGAGGTCGGC 1703	ם
GGACT	Ø
Db 1584 GACGAGCGGCACGACGCGTCACGGTCATGGTCGGCTTCGACGACGACTTCCCGCAG 1643	ם
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Db 1524 CCCGACACGGCCGGCCCGGCCTCCACGCTCCTCGCCGCCGACGGCACCGTCCTC 1583	D
GGGCATGCGCTGGAGGGTCT	Ø
Db 1464 GTCGACGGCGTCGACGCTCCGCCCCCGTGCCCCGCGCGCCCGGGTTCGTCGTGGAC 1523	U
Qy 1464 ACCGTCGGCGCCTACACCACCGTTCCTCCCATTCTAGGCGAGCAGTGCCTCACGCCCGAC 1523	۵
Db 1404 CCGTACCAGGTGAGCGTCGCCGAGGGCCTCACCGCGCTGCTCGGCGACGCGGTCGACGTC 1463	D
Qy 1404 TACTACGCAGTCACTCCCTTTGACGGCCTCAGCAAGCAGCTCGAGACGCCGCCATCGTAC 1463	۵
Db 1344 GTCGGGCGCACGCGCTCGAGACGATCGACATGGGCGGCGGCTCCGCGGACCGTCAACCCG 1403	;
Qy 1344 GTCGGCCCCAACGCCAAGCAGGCCACATACCACGGCGGAGGCTCTGCCGCACTCAGGCC 1403	ю
Db 1284 ACCGTCCTCACCAACGCCGACGACACCCTGCCGCGCGCGC	D
Qy 1284 GTGCTGCAGAGAACGAGAACGTTCTGCCCTTGAGCAAGAAGAAGAAGAAGACGCTGATT 1343	0
Db 1224 CCCGCCCCGACAGCGCCGTCCGGCGCGAGCAGCTCACGCGCCTCGCCGCCGCCGCCATG 1283	п
Qy 1224 ACTGTCAACAACACCCCCGGAAACGGCAGCTCTCCCGGAAGGTTGGCAACGAGGGCATC 1283	2
	п
Qy 1167 CTTCAGTTCGTCAAGAAGTGTGCCTGCCTCCGGAGTGACGGAGAACGGCCCCGAGACG 1223	n
Db 1104 GCCGCCGTGCGCAGCGAGCTCGACGAGCTCGTCGACCACCTGCGCCGCCTG 1163	п
Qy 1107 TTCAACGTCTCCAACGGAAAGCCCTTTATCCACGTCATTGACCAGAGGGCTAGGGAAGTT 1166	n
Db 1044 GCCGGCGGCCTCGACCTCGTCATGCCCCGGGCCCACGGCCCCTGGGGCGACGCGCTCGTC 1103	н
Qy 1047 GTGGCAGGCCTCGAGCTCGAGATGCCCGGACCTCCACGCTTCCGAGGAGAAACACTCAAG 1106	2
Db 984 GCTACACCGGCCTCGTCATGTCCGACTGGTTCGCGACCCGGACCCGCACCCGCCCCC 1043	н
Qy 987 GGTTGGGATGGCCTAATCATGAGCGACTGGTACGGCACATACAGTACCACAGAAGCCCTT 1046	~
Db 924 AACGGCGTCCCCCGCGAGCACCACCACGTCGTCAACGAGGTCCTCAAGGGCGAGGTGG 983	н
QY . 927 AATGGCGTGTCGTGCAGCGAGAACCCTAAATATCTTGATGGGATGCTTCGAAAGGAATGG 986	_
864 TTCGAGATCGCCGTCGACGAGTCCGACCCGTGGTCCGTCATGGCCGCGTACAACGACGTC 9	_
867 TTCCAGATTGCTGTGCGAGACTCCCAGCCGGGTGCCTTCATGACGGCGTACAATGCCCATC 92	_
804 CGCAACACCATGAACTCCGTCGTCGACCCCGCGACGCTCCGCGAGCTCTACCTGCCGC 8	_
GCATGATGGTGCAGAGCATCGTCACGGAGCGGGCTCTCCGTGAAATCTACGCACTCCCG	^
Db 744 CAGGACCTCGGCGTCGGCCTGCCTCAAGCACCTCGTCGCCAACGAGTCGGAGACCGAG 803	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCGTGACCGTCGGCGACGCCGACCCGGCACGCGGGGGGCGCCGCCGAGCCGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCGGCCAGGAGGGCGGCCGCGTGGCCGCCGCCGCTGCTCGGCGACCAGGAGCCGACC 2303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACGCGCTCGTGCGGGCCGTCGCCGCGGCCGCCGCACGGTCGTCGTCGTCAACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACCAGCTCATTGCCGACGTGGCCGCCGCGAACCCCAAACACCGTCGTCGTCATGCAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCGAGGAGGAGGACGAGTCCGTCGACAAGTCCACGATCGCGCTGCCCGGCGCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACGCCGACTGGGAGACCGAGGGCGCGCGACCGCGGGGAGCATGAAGCTCCCCGGCGTGCTG
                                                                                                                                                                                                                                                      CCCGGCGAGACG
                                                                                                                                                                                                                                                                                  TCCGACGAGCCCGTGCGCCTCGTCGGCTGGGCCGACGCGACCGTCGACGCCGGGGGGGTCC 2663
                                                                                                                                                                                                                                                                                                                                             ACCAACACCGGCGCGCGCACCAGCCGCGAGGTCGTCCAGGTCTACCTGGAGCCCGCGTCG
                                                                                                                                                                                                                                                                                                                                                            AAGAACACCGGCTCCGTGCCCGGCGCACAGGTGGCCCCAGCTCTACGTCAAGCCCCTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                        GCCTTTTCCAATCTCTCCGTGTCTCACAAGGACGGCAAGCTGAGCGTGTCCCTCTCCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCGACCGGGCGCCCGCGCGTTCTGGCTCGGGCACGGCCTCGGGTACGCGACGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGTTTGCCGACAAGGACGTCAATTTCCCCCTTTGGCCACGGCCTGTCCTACACCACTTTT 2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCGTCGACGGCGACCTGGAGTACACCGAGGGCCGGTTCGTCGGCTACCGCGGCCACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGGCAACGAGACGGCCAACTCCATTGCCGACGTCGTCTTTGGCGACTACAACCCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGACGCCGGTGCTCATGCCGTGGCTCGACGACGTCGACGCCGTGCTGTGGGGCCGGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCGAAAAGTCCGTCGCCCTCGCCAAGGAGCACGACCAGGTCATCATCTGCGCGGGCCTT
                                                                                                                                                                                                                        GCCCGCGTCACG
                                                                                                                                                                                                                                                                                                             GCGGCCAAGATTAACCGCCCCGTCAAGGAGCTCAAGGGCTTCGCAAAGGTCGAACTGCAG
                                                                                                               A.tumefaciens beta-D-glucosidase (cbg-1) gene, complete cds
M59852
                                                      Agrobacterium tumefaciens
                                                                      A.tumefaciens DNA.
                                                                                    beta-D-glucosidase.
                                                                                                  M59852.1 GI:142221
                            Rhizobiaceae; Rhizobium.
                                        Bacteria; Proteobacteria;
         (bases 1 to 3710)
                                                                                                                                                                                                                        2675
                                                                                                                                                                                                                                                      2654
Smith, K.D. and
                                                                                                                                              3710 bp
                                          Alphaproteobacteria; Rhizobiales;
Morris, R.O.
                                                                                                                                                BCT 26-APR-1993
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 1195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
485 TTCACCGCTCCGGCCTCAATGGCCGCAACTTCGAATGCTATTCGGAAGAQCCGGCGCTGA
                                                                                                                                                                                                                                                                                                                                                                             475 GCCCCAACGGCGTAAGAGGGACCAAGT---TCTTCAATGGCGTCCCTGCGGCCTGCTTCC
                                                                                                                                                                                                                                                                       532 CTTGCGGCACGTCGCTCGGTTCCACATTCAACCAAACTCTGCTCGAAGAGGCAGGTAAGA 591
                                                                                                                                                                                                                                                                                                                          305 GCCCCAATGGCGCACGCGGCGGCGGGTCGCTGGTCGGCGGCGTCAAGTCCGCCTGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                      245 ATTTCTGGACGACCGTCGCGATCGAGCGGCTCGGCGTGCCGAAGATCAAGGTTACCGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 TCGACGATATTCTCGATAAGATGACACTGGAGGAGCAGGTGTCGCTGCTCTCGGGCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  652 TGCAACGCTCCCCTCTCGGTGGACGTGGCTTCGAGTCGATTGGTGAGGATCCGTTCCTGG
                                                                                                                                                              592 TGATGGGCAAAGAGGCCATCGCTAAGAGTGCGCATGTGATCCTCGGCCCGACTATCAACA
                                                                                                           CGCTGGGAGGACAAGCCAAGAGCAAGGGCGCGTCGGTGCTTCTGGCGCCCGACCGTCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTTCTGGCACACAAAGGCTCTCCCCAAGCATGGAGTCCCCTCTCTCCCGCTTTACAGATG
                                                                                                                                                                                                                    CGGTGGCAATCGCGCTTGGAGCGACGTGGGACCCCGGAGCTCATCGAGCGGGCCGGCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 174 (5), 1478-1486 (1992) 92165721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning and sequencing of an Agrobacterium tumefaciens beta-glucosidase gene involved in modifying a vir-inducing plant signal molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1537792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Translation="MIDDILDKMTLEEQVSLLSGADFWTFVAIERLGVPKIKVTDGPN
(CARGGGSLVGGVKSACEPVALTACAVALTGEQAKSKCASVLLAPTVNI
HRSGLNGRNFECYSEDPALTAACAVALTINGVOSGGVAATIKHEVANBSETERROTMSSD
VDERTILREIYLPFEEAVKKAGVKAVMSSYNKINGTYTSENPWLLTKVLREEMGFDGV
VMSDWFGSHSTAETINACLDLEMPGPWRDRGEKLVAAVREGKVKAEGVKASSARIILLL
LERVGAFEKAPDLAEHALDLPEDRALIRQLGBEGAVLLKNOGVLPLAKSSEPOJAVIL
LERVGAFEKAPDLAEHALDLPEDRALIRQLGBEGAVLLKNOGVLPLAKSSEPOJAVIL
ERVGAFEKAPDLAEHALDLPEDRALIRQLGBEGAVLKNOGVLPLAKSSEPOJAVIL
ENAASAKVMGGGSARIAHYTVSPLEGIRAALSNANSLRHAVGCNNNRLIDVFSGEMT
VEYFKGRGFESRPVHVETVEKGEFFWFDLPSGDLDLADFSARMTATFVPQETGEHIFG
MTNAGLARLFVDGELVVDGYDGWTKGENFFGTANSEORRAVTLGARARRYMVYEYEAD
KASLDGINICALRFGVEKPLGDAGIAENVETAKKDIVLLLVGREGEWDTEGLDLPDH
RALPGROEELIEAVAETNPNVVVVLQTGGFIERWFUKGKVRAVLQWWYPGQELGANALADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFGDVEPAGRLÞQTFÞKALTDNSAÏTDDÞSIYÞGQDGHVRYAEGIEVGYRHHDTREIE
ÞLFÞFGFGLGYTRFTWGAÞQLSGTEMGADGLTVTVDVTNIGDRAGSDVVQLYVHSÞNA
RVERÞFKELRAFAKLKLAÞGATGTAVLKIAÞRDLAYÞDVEAGRFRADAGKYELÍVAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="beta-D-glucosidase"
/protein_id="AAA22082.1"
/db_xref="GI:142222"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="cbg1"
181. .2637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="cbg1"
169. .173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_lib="genomic HindIII cosmid"
169. .2637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:358"
/cell_line="B3/73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIDIRASVSIHLPVDHVMEP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="active site"
1084 c 1168 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Agrobacterium tumefaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="cbq1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /EC_number="3.2.1.21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="cbg1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 343.4; DB 1; Pred. No. 9.7e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69;
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        544
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8;

792 CCGGCGATGCCTTCTTCGGCTCCGCCACCCGCGAGGAGACGGGCCGCATCAATCTCGTCA 185	Qy 1
	_
732 GCACGGCAAAGGCGTACGTAGACGACCAGCTCGTCGTCGACAACGCCCACCAAGCAGGTCC 1	0у 1
	Db 1
672 TGGAGGGCACGTACACCGCCGACGAGGACTGCACCTACGAGCTCGGCCTCGTCGTCTGCG 1	Qy 1
ATTOTTCTGGTTCGGTCTCGGTCCGGCGACCTTGATCTCGCCGCATTTTTCGGCGCGCCA	<u></u>
612 CGGACATGCACCTGGTGGACTACTACCACCCCAAGGCGGCAGACACGTGGTACGCCGACA 167	Qy 1
64 ACTTCAAGGGACGCGGCTTCGAGAGCCGTCCGGTCCATGTCGAGACCGTCGAAAAGGGCG 1	ъ
	Ωу 1
	Db 1
492 CCATTCTAGGCGAGCAGTGCCTCACGCCCGACGGCGCTCCGGGCATGCGCTGGAGGGTCT 15	0у 1
432 TCAGCAAGCAGCTCGAGACGCCGCCATCGTACACCGTCGGGGGCCTACACCACCGCTTCCTC 149	Qy 1 Db 1
205 T	Db 1
372 AC	Qy 1
	Db 1
312 T	Ωу 1
1252 CTCTCCTCCGGAAGGTTGGCAACGAGGGCATCGTGCTGCTGAAGAACGAGAACAACGTTC 1311	Qу 1 рь 1
025 c	Db 1
192	Qy 1
965 AGGCCGAGACCGTGCGCCTTCGGCACGCGTATTCTCCTTCTGCTCGAACGCGTCGGCG 102	ДЪ
132	Qy 1
905 CGGGGCTTGGCGGGATCGCGGCGAAAAGCTGGTCGCCGCAGTCCGGGAAGGCAAGGTAA 9	Db
072	Qy 1
845 ACTGGTTCGGCTCGACGCCTGAAACCATCAATGCCGGGCTCGATCTGGAGATGC, 904	Дb
1012 ACTGGTACGGCACATACAGTACCACAGAAGCCGTTGTGGCAGGCCTCGACCTCGAGATGC 107	Qy
785 CCTGGCTGACGAAAGTCCTGCGCGAGGAATGGGGCTTCGACGGCGTGGTCATGTCCG 844	DЬ
952 CTAAATATCTTGATGGGATGCTTCGAAAGGAATGGGGTTGGGATGGCCTAATCATGAGCG 101	Qy
725 GCGTGAAGGCCGTCATGTCCTCCTACAACAAGCTCAACGGCACCTATACGAGCGCAAAATC 7	ФФ
892 AGCCGGGTGCGTTCATGACGGCGTACAATGGCATCAATGGCGTGTCGTGCAGCGAGAACC 9	Qy
665 ATGAGCGGACGCTGCGCAAATCTATCTGCCGCCTTTCGAGGAGGCCGTGAAGAAGCCCG 7	Дb
832 CGGAGCGGGCTCTCCGTGAAATCTACGCACTCCCGTTCCAGATTGCTGTGCGAGACTCCC 891	Qy
05	Db 2
	OV
545 CCGCCGCCGCCGCCGCCATATATCAATGGCGTGCAGAGCCAGGGTGTGGCCGCCACGA 604	Db
712 CGGGCTTGGGAGCTGCGGCTCTCATCCGCGCGCATTCAGAGCACTGGAGTGCAGGCTACGA	Qy

RESULT 9
ABI293760
ABI293760
ABI293760
LOCUS
ABI293760
DEFINITION Agaricus bisporus mRNA for putative beta glucosidase (bg1 gene), strain D649.

Qy 2495CGGCAAGCTGAGCGTGTCCCTCTCCGTGAGAGACACCCGGCTCCGGCGCAC 2550
2495CGGCAAGCTGAGCGTGTCCCTCTCCGTGAAGAACACCGGCTCCGTGCCGGGCAC 2506 GGGCGGATGGTCTTACGGTGAACGGTCGATGTCACCAATATAGGCGACAGGGCGAACGGCGGATCGG 2551 AGGTGGCCCAGCCTCTACGTCAAGCCCCTCCAAGCGCCAAGATTAACCGCCCCGCCCAAGG [
2495CGGCAAGCTGAGCGTGTCCCTCTCCGTGAAGAACACCGGCTCCCGGCGCAC
2495CGGCAAGCTGAGCGTGTCCCTCTCCGTGAAGAACACCGGCTCCGTGCCGGCGACCGCCAC 2306 GGGCGATGGTCTTACGGTGACCGTCGATGTCACCAATATAGGCGACAGGCGGGATCGG 2551 AGGTGGCCCAGCCTCTACGTCAAGCCCCTCCAAGCGCCAAGATTAACCGCCCCGCCAAGG [
2495CGGCAAGCTGAGCGTGTCCCTCTCCGTGAAGAACACCGGCTCCCGGGCGCAC 2306 GGGCGGATGGTCTTACGGTGAACACGGTCAAGATATAGGCGACAGGGCGGGATCGG 2551 AGGTGGGCCAGCTCTACGTCAAGCCCCTCCAAGGGCCAAGATTAACCGGCCCGGTCAAGG 1
2495CGGCAAGCTGAGCGTGTCCCTCTCCGTGAAGAAACACCGGCTCCCGTGCCCGGCGCAC
2495CGGCAAGCTGAGCGTGTCCCTCTCCGTGAAGACACCGGCTCCCGTGCCCGGCCGCCAC 25 2306 GGGCGGATGGTCTTACGGTGACCGGTCGATGTCACCAATATAGGCGACAGGCGGGATCGG 23 2551 AGGTGGCCCAGCTCTACGTCAAGCCCCTCCAAGCGGCCAAGATTAACCGCCCCCCCAAGG 26
2495CGGCAAGCTGAGCGTGTCCCTCTCCGTGAAGAACACCGGCTCCCGTGCCCGGCGCAC 25
2495cggcaagcTgagcgTgTcccTCTccgTgaagaacaccggcTccgTgcccggcgcac 25
Db 2246 TCGGTCTTGGCTACACCCGCTTTACCTGGGGTGCCCCGCAACTATCGGGAACGGAAATGG 2305
QY 2440 ACGGCCTGTCCTACACCACTTTTGCCTTTTCCAATCTCTCCGTGTCTCACAAGGA 2494
Db 2186 TCTTCGTCGGCTATCGCCATCACGATACAAGAGAGATCGAACCACTCTTCCCCTTCGGCT 2245
QY 2380 TCTACGTCGGGTACAGGTACTACGAGTTTGCCGACAAGGACGTCAATTTCCCCTTTGGCC 2439
Db 2126 TTACCGACGATCCGTCGATCTATCCTGGCCAGGACGGCCATGTGCGCTACCCGGAAGGGA 2185
Qy 2332 TTCTCAACTTCCGCAC
Db 2066 TCGAGCCTGCCGGCCGCTTGCCACAGACCTTCCCGAAGGCGCTCACGGATAATTCCGCCA 2125
Qy 2272 ACAACCCCTCGGGCAAGCTGTCCCTCAGCTTCCCCAAGCGCCTGCAGGACAACCCCGCGT 2331
Db 2006 AGATGTGGTATCCCGGCCAGGAACTTGGCAATGCGCTTGCGGACGTTCTCTTTGGTGATG 2065
Qy 2212 AGGCCTGGTACGGCGCAACGAGACGGGCAACTCCATTGCCGACGTCGTCTTTGGCGACT 2271
Db 1946 TACTGCAAACGGGTGGTCCCATCGAGATGCCATGGCTCGGCAAGGTGCGTGC
Oy 2152 TCATGCAGACGGGCACCCCCGAGGAGATGCCCTGGCTCGACGCCCACGCCGCCGTCATCC 2211
Db 1886 CGGGTCGCCAGGAGGAGCTGATCGAGGGGTCGCCGAAACCAATCCCAACGTGGTCGTTGG 1945
Qy 2092 CCGGCGTGCTGGACCAGCTCATTGCCGACGTGGCCGCCGCGAACCCCAAACACCGTCGTCG 2151
Db 1826 TCGTCGGCCGTGAGGGCGAGTGGGACACCGAAGGTCTGGATCTGCCCGACATGCGCCTGC 1885
Qy 2032 GCGCGGGCCTTAACGCCGACTGGGAGAGCCGAGGGGGGGCGCGAGCGGGGGGGAGCATGAAGCTCC 2091
Db 1766 GCGATGCCGGGATTGCGGAGGCGGTCGAAACCGCCCGCAAGTCCGATATCGTACTGCTCC 1825
Qy 1972 ACCAGGCCGAAATCGAAAAGTCCGTCGCCCTCGCCAAGGAGCACGACCAGGTCATCT 2031
Db 1709 CCAGCCTGGACGGATCAACATATGTGCGCTCCGGTTCGGATGCGAAAAGCCGCTCG 1765
Qy 1912 GCGACACCATCGTCCCCGGCCACGGCTCCCTCCGGCGCCGGCGGCTGCAAGGTCATTGACG 1971
Db 1664 CCGCACGCCGCTACCGGGTTGTGGTCGAATATGAGGCGCCCGAAGG 1708
Qy 1852 AGGGCAACACGTACAAGTTCAAGATCGAGTTCGGCTCCGCACCCACC
Db 1604 AGGGTGAGAACTTTTTGGAACCGCGAACAGCGAGCAGCGTCGGGCGGTAACGCTTGGGG 1663

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REFERENCE
AUTHORS
TITLE
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                                             509 TGGCGTCCCTGCGGCCTGCTTCCCTTGCGGCACGTCGCTCCGGTTCCACATTCAACCAAAC
                                                                                                                                                                                          90 AGCCATTCTTTTGAGTGCCGGAGTTGGATTTTGGCATACTCATGCAATTGAGAGGCTGCA 149
                                                                                                                                                                                                                                                                                  TCCCTCTGACTTTGCCAACGCTGACATTGATAAAATTGTCGACGCATTGACTACCGATGA 89
                                                                                             GATTCCCGCTGTGAAGGTTAGCGACGGCCCAATGGTATCCGAGGAAATCATTTCTTTAT 209
                                                                                                                                                                                                                                       GAAGGTCGATCTGCTGGCTGGTATCGACTTCTGGCACACAAAGGCTCTCCCCCAAGCATGG 448
  GGGCACGCCAGCCAAGTGTTTGCCGTCATCCACTGCAATGGGCGCAACTTTCGATCGTGA 269
                                                                                                                                             AGTCCCCTCTCTCCGCTTTACAGATGGCCCCAACGGCGTAAGAGGGGACCAAGTTCTTCAA 508
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Agaricaceae; Agaricus.
1 (bases 1 to 2636)
Morales-Almora,P. and Thurston,C.F.
Molecular analysis of the cellulolytic genes in Agaricus bisporus
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AJ293760.1 GI:9796011
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Agaricus bisporus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            College London, 150 Stamford Street, London,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-AUG-2000) Morales-Almora P., Microbiology, King's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morales-Almora, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEDVPAHGYFHSEKGKVTYAEGLYVGYKHYQHRNIEPLFAFGHGLSYTSFNISDLRLS
QPIVSGDQFDLKATVKLTNTGNITGSQVVQLYIGLPKTSELTHPRWQLRGFKKMRDVK
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VEFFGCGSEEETGVVELKAGVKHEIYVDFCNVRGPADGDETETIMDSNPGIRLGGAEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPLDRKSLKKVAIVGGNAKAAVLSGGGSAALKPSYFVARPAGLVKALKEVNPNIEVTY
SEGARAAKTLPTLDFDLFTESGORGWTGSWHAHE,NDDSLVALPTPIKTOYVDETTMFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVKVSDGPNGIRGNHFFMGTPAKCLPSSTAMGATFDRDLLEEVGLKLLAREAKLRSAS
VILAPTCNIQRNPLGGRSFESFSEDPFLSGMLCSAYINGIQKGGIGATIKHFVGNDKE
DDRTGYDSIHYRTTSSGDLSPSVHAGSRNMPLHGAINTAYNRVNGIHVCENPELLQKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative beta glucosidase"
/protein_id="CAC03462.1"
/db_xref="GI:9796012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="bg1"
25. .2610
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/clone="PMRT1615"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAVVVTQAGSAITMPWVDQVSSLLHTWYLGNATGDAIADVIFGNHNPSGKLSLTFPKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDPDELLNSAVSIAKDADAVIIVVGLNGDWETEGNDRTTLALPGRTDELVQKVVAANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRDEWKSDYMIMSDWFGTYSVDVGLNAGLDLEMPGLNKWRSLESVNRSIQSRKVTAKK
VKERARKVLELVKKCAQGAPEILDGDGLERTLDSDEDNALMRKFAAESIVLLKNDKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Agaricus bisporus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGESREVELVMDRLSVSYWDKEWVVENGAYDVRVAFTSEEGVGEGQELLGRFNVEKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /country="United Kingdom"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="D649"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MPPSDFANADIDKIVDALTTDEAILLSAGVGFWHTHAIERLQIP/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function="putative hydrolysis of beta-D-glucose"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGAGGGCATCGTGCTGCTGAAGAACGAGAACAACGTTCTGCCCCTTGAGCAAGAAG-----
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                                                                     TGGAGGGTCTTCAACGAGCC----CCCTGGTACCCCTAACCGCCAGCACATTGACGAGCT 1597
                                                                                                                             ACCGACTTTGGATTTCGATTTGTTCACTGAGTC-CGGCCAACGTGGCTGGACTGGGTCTT
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                                                                                                                                                                   ACCGTTCCTCCCATTCTAGGCGAGCAGTGCCTCACGCCCGACGGCGCTCCGGGCATGCGC 1541
                                          GGCATGCTCATGAAAATGACGATAGCCTCGTTGCCTTGCCTACGCCGATAAAAACACAAT 1348
                                                                                                                                                                                                                                                                                                TGCTGCCCTCAAGCCGTCCTACTTCGTCGCGGCGGCCGGGCCGGGCTGGTCAAGGCTCTGAA 1169
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                                                                                                                                                                                                                                                                                                                                               GCGAGGACGTCTACGTCGGGTACAGGTACTACGAGTTTGCCGACAAGGACGTCAATTTCC
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                                                                                                                                                       fragments
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48.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   945 GAGAACCCTAAATATCTTGATGGGATGCTTCGAAAGGAATGGGGTTGGGATGGCCTAATC 1004
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GCGCAGGTGATGGGAGGCGGCTCGGCGCAGTTGAACCCTCACTATGTCATCAGTCCGTGG
                                              GCCACATACCACGGCGGAGGCTCTGCCGCACTCAGGGCCTACTACGCAGTCACTCCCTTT 1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGCCCTTTATCCACGTCATTGACCAGAGGGCTAGGGAAGTTCTTCAGTTCGTCAAGAAG 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGATGCCGGGCCCGACTCGCGATCGCGGCTCCAAGCTACTGGCTGCGGTCGAAGGCGGC 80370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGTCGGACTGGTTCGGCGTTCGACCGCACCCGTGAATGCCGGGCTGGATCTG 80430
                                                                                                     -----CTGCCATTGGCTCAGCAAGGTATGGTCGCCATCATTGGACCCAATGCCAAGGTC
                                                                                                                                                 AACGTTCTGCCCTTGAGCAAGAAGAAGAAGACGCTGATTGTCGGCCCCAACGCCAAGCAG
                                                                                                                                                                                                    AGGGCATTGATCAGGCGCGCGGGAGCGGAAAGCGCAGTTCTGCTACAGAATGACGGGATC
                                                                                                                                                                                                                                                        ACGGCAGCTCTCCTCCGGAAGGTTGGCAACGAGGGCATCGTGCTGCTGAAGAACGAGAAC 1304
                                                                                                                                                                                                                                                                                                          ACCGGCGCTATCAACGATCATCGCGAGTTTAAGGAGTACGCCATTGATCAACCGAAACAT 80250
                                                                                                                                                                                                                                                                                                                                                        TGTGCTGCCTCCGGAGTGACGGAGAACGGCCCCGAGACGACTGTCAACAACACCCCCGAA 1244
                                                                                                                                                                                                                                                                                                                                                                                                         GAGGTTAGTGTCGAGACGATCCGCGCCTGTGTGCGCAATATCCTGACTTTGATGGAACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBMED
      CDS
                                                                    gene
                                                                                                                                  stem_loop
                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                               sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 8AG lies between 3F9 and 1F2 on the Aser-A genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prediction is based on positional base preference in codons using specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-JUL-1998) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in codons is given for each CDS.

Usually the highest scoring match found by fasta o is given for CDS which show significant similarity to other CDS in the database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Details of S. coelicolor sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by the BBSRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor A3(2). Streptomyces coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthetase alpha chain; succinyl-coa synthetase beta chain; succ); TPP-requiring enzyme; transfer-RNA-Leu; TTA Leu codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8843436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 37445) Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta-glucosidase; elongation factor G; fusA; sucC; succinyl-coa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinashi, H. and Hopwood, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      set of ordered cosmids and a detailed genetic and physical map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 37445)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 37445)
                                                             complement(730.
                                                                                                                                                          nominal overlap with cosmid
                                                                                         /note="hairpin loop with 23 bp stem"
                                                                                                                                                      /note="nominal overlap with St8A6 from 1 to 106 nominal overlap with cosmid 3F9 from 19725 to 19830"
                                                                                                                                                                                                                                                                                            /db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                           /strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                               /organism="Streptomyces coelicolor A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                             'clone≖"cosmid 8A6'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Harris,D
                                                             .2160)
.2160
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CDS gene

complement(4382. .5614) /gene="SCO6583"

/note="SC8A6.04c, probable transferase, len: 410 aa; highly similar to TR:006644 (EMBL:U82167) formy1-CoA transferase from Oxalobacter formigenes (428 aa), fasta scores; opt: 95 4 z-score: 1732.0 E(): 0, 50.7% identity 1428 aa overlap. Also similar to many dehydratases e.g. CALB.ECOLI L-carnit ine dehydratase (EC 4.2.1.89) (405 aa), fasta scores; opt: 285 z-score: 317.7 E(): 1.9e-10,

26.2% identity in 427 aa o verlap

misc_feature

```
/note-"SCBA6.03c, unknown, len: 714 aa; similar to many hypothetical proteins including several from each of the arche ons Archaeoglobus fulgidus TR:028341 (EMBL:AE000970) conser ved hypothetical protein AF1938(673 aa), fasta scores; opt: 960 z-score: 1289.8 E(): 0, 35.6% identity in 693 aa overla pa and pyrococcus horikoshii D1028624 (EMBL:AB009518) hypothetical protein PHCV016 (460 aa), fasta scores; opt: 1280 z -score: 1246.9 E(): 0, 44.3% identity in 461 aa overlap. Co ntains PS00216 Sugar transport proteins signature 1. Also s imilar to S. coelicolor hypothetical protein SC9B10.09 (E(): 6.1e-15, 23.0% identity in 347.4.1% in 278.2.
                                                                                                                           complement(3340. .3387)
/gene="SCO6582"
                                                                                                                                                                                                   VTDNGLSLMEIPPDLDRAFRAFIPPFGAAGNPVDITGGEPPSTYEATIRLGLEDPRIH
ALVLGYWHTIVTPPMVFAELTARVVAEFRERGVEKPVVASLAGDVEVEEACQYLFERG
VVAYYYTTEKEVAVLGAKYRWARAAGLLGGGS"
                                                                                                                                                                                                                                                                                                                                                            VIATEBGAVAADIRVILATDIPKERRRYTREEILTSMRRLMQPASVAVIGASGEPGKI
GNSVMRNLVDGGFAGE HPVNPKADDILGRKAYKSVTDVPGEVDVAVFA IPARRYVAAA
LEEVGRKRIPHAVLIPSGFAETGEQALQDEIVAAVAERHGVRLLGPNIYGYYSTMODLG
ATFCTPYDVKGGVALTSQSGG IGMA ILGFARTTKTGVSAIVGLGNKSDLDEDDLLTDF
GEDPHTECIAMHLEDLKDGRAFYEAARATVPRKPVVVLKAGRTAAGAKAAGSHTGALA
complement(4382. .5614)
/gene="SCO6583"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LARDVDEAVACAARFGGPVVMKIVSPDILHKTDAGGVVVGYEGAADVRAAFCRIVDNA
RAYDASARIEGVQIQELLPQGQEVIVGAVTDPTFGKVVAFGLGGVLVEVLKDVTFRLA
PVDADEALSMLDSIRAAEVLRGVRGQAGVDRWAVAEQIRRVSELVADFPEIAEVDLNP
                                                                            /note="PS00216 Sugar transport proteins signature 1"
                                                                                                                                                                                                                                                                                                                          GDDAVYDDILRQAGVIRAPGLNEMLEYARALPVLPAPEGDNVVIITGAGGSGVLLSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(2233. .4377)
/gene="SCO6582"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VALSLRPPGRPKGKRVTPNPQPLGEG
complement(2233. .4377)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="SC8A6.02c, probable transmembrane transport protein, len: 476 aa; some similarity to e.g. TR:051330 (EMBL:04007 5) oxalate:formate antiport protein from oxalobacter formig enes (418 aa), fasta scores; opt: 22 z-score: 230.1 E(): 1 .4e-05, 24.1% identity in 436 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MAEDRLARVRGLLDAVRGEGRTALTAPEGKVLADAYGIAVPGEE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:087837"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="conserved hypothetical protein"
/protein_id="CAA19775.1"
/db_xref="GI;3288603"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.9% identity in 375 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVFLAAMVAIAGFYFRDPPKNWWPAAVDPLNPPADPRARRSLEKNPPAVKQYSPMEAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CQAAVAFPAGRLRESGKLPARWAMMLGSAGTLLGYLSLAFAPHVSLAFIGFGVFSGMG
AGMYYATCVMMVGKWYPERRGGKTGFVNGGFAYGSVPFVFIFHGYMDTSNFRWVLVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDIDLMGRKRKWMVILPWIGMMGISSAEYAFASAEDTLHEAQHWSSGSIYWMMTAWVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTADYFGENNNATNYGMYYSSKLVSGLGAGMGSVVVGV\\\GYNGAFSLAGSISIFAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GWLSDLYGRKQCLLYVCAILGLAQFGIIWSAEIKNLPLFLYFSAISGFGGGAIFPMFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTGRVALMWFCLACTSGVNIFGIAFQVDIGEEAGFAAGVŸAAAMSLKAIVNGTGRGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SC06582"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative transmembrane transport protein"
/protein_id="CAA19774.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MGQGALARSFDARGAIDMTTTDVTRVAAYREVTDRNGRVYRVGE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SPTREMBL:087836"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:3288602"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="SC06581"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
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gene

gene CDS

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Best Local Similarity Matches 1152; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27611 AAGCTGACCACGCGCCCCGCGCACTGCTGCTGAACGGCGCCACGACCTGGCGCACGAGG 27670
                                                                                                                                                                                                                             27731 GGCGAGGCCTGGGACGAGCGAGCACCTCTCTCCTGCTGCCCTCCGCCTCGGCGCTCGCC 27790
                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 AAGCTCACCCTGGCCGAGAAGGTCGATCTGCTGGCTGGTATCGACTTCTGGCACACAAAG 431
                              612 GCTAAGAGTGCGCATGTGATCCTCGGCCCGACTATCAACATGCAACGCTCCCCTCTCGGT 671
                                                                                                                                                                TCCACATTCAACCAAACTCTGCTCGAAGAGGCCAGGTAAGATGATGGGCCAAAGAGGCCCATC 611
                                                                                                                                                                                                                                                                                           GGGACCAAGTTCTTCAATGGCGTCCCTGCGGCCTGCTTCCCTTGCGGCACGTCGCTCGGT 551
                                                                                                                                                                                                                                                                                                                                                                                                                            GCTCTCCCCAAGCATGGAGTCCCCTCTCTCCGCTTTACAGATGGCCCCAACGGCGTAAGA 491
                                                                                                  GCCACCTGGGACGAGGCGCTGGTCGAAGACCTCGGTGGCCTGCTCGCCGCCGAGGCCCGG 27850
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"SC886.05c, probable TPP-requiring enzyme, len: 560 a ; similar to many e.g. ILVB_MYCTU probable acetolactate synthase (EC 4.1.3.18) (547 aa), fasta scores; opt: 733 r-sco re: 1305.6 E(): 0, 36.4% identity in 557 aa overlap. Contai ns 9500187 Thiamine pyrophosphate enzymes signature and Pfam match to entry PF00205 TPP_enzymes, Thiamine pyrophosphate enzymes, score 343.90, E-value 5e-106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAQIGDSGTGVHVVAGILAALYQREHTGRGQRVNVAMQHAVLNLCRVKLRDQQRLS
HGPLAEYPNEDFGDEVPRSGNASGGGQPGWAVKCAPGGPNDYVYVIVQPVGWQPLSEL
IGRPELAEDPEWATPRARLPKLNKMFQLIEEWSSTLPKWEVLERLNAHNIPCGPILST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(5623. .5627)
/note="possible RBS upstream of SC8A6.04c"
complement(5628. .7308)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MTAKALEGIRVLDMTHVQSGPSATQLLAWLGADVVKLEAPHGDI
TRGQLRDLPDVDSLYFTMLNCNKRSITLNTKSERGKEILTELLRRSDVMVENEGPGAV
DRMGFTWDRVKEINPRIVYASIKGFGEGPYTAFKAYEVVAQAMGGSMSTTGFEDGPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative transferase"
/protein_id="CAA19776.1"
/db_xref="GI:3288604"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
/product="putativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(5683. .7254)
/gene="SCO6584"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mpDDTQDvISGGHLVAKALKAEGVDRIYTLCGGHIIDIYDGCVD
EGIEVVDVRHEQVAAHAADGYARITGKPGCAVVTAGPGTTDAVTGVANAFRAESPMLL
IGGQGAHTQHKMGSLQDLPHVDMMTPITKFAATVPDTARAADMVSMAFRECYHGAPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative TPP-requiring enzyme"
/protein_id="CAA19777.1"
/db_xref="GI:3288605"
/db_xref="SPTREMBL:087839"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(5626. .7308)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (5962..6021)
/gene-"SC06584"
/note-"ps00187 Thiamine pyrophosphate enzymes signature"
complement (7316..7319)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Pfam match to entry PF00205 TPP_enzymes, Thiamine py rophosphate_enzymes, score 343.90, E-value 5e-106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INGGAAKRKEWLDELRAAERTALDKRLPQLRSDASPIHPYRLVSEINDFLTEDSIYIG
DGGDIVTFSGQVVQPKSPGHWMDPGPLGTLGVGVPFVLAAKQARPDKEVVALFGDGAF
SLTGWDFETLVRYDLPFVGIVGNNSSMNQIRYGQAVKYGKERERVGNTLGDVPYDEFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQVWTTRATEAAVELVRTLNVPAYMNGAGRGTLPPGDPHHFQLSRRYAFSNADVIVIV
GTPFDFRMGYGKRLSPDATVVQIDLDYRTVGKNRDIDLGIVGDAGLVLKSVTEAASGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFLEIPRDVLDAKVPAEKARVPRAGGYRASTRSAGDPEAVERLADLLVHAEKPAVLLG
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700	5 CCCCCACTGGACCCGGACACATGCACCGACCCGCGCTCGGGGCTGCCCCGCGCTCCTCCTCCTC	Db
1650	ACGAGETETTETEACCAAGACGGACATGCACCTGGTGGACTACCTACCACCCCAAGGCGG	Qy
1590 28864	1533 GGCATGCGCTGGAGGGTCTTCAACGAGCCCCCTGGTACCCCTAACCGCCAGCACATTG	Qy Db
1532 28804		Qy Db
7	1416ACTCCCTTTGACGGCCTCAGCAAGCAGCTCG-AGACGCCGCCATCGTACACCGTCGGC	Qy Db
1415 28684	O ,	Qу
28624	565 GGTGCGAAGCCGTCCGGGCCCCGACCGCGGCGTGCCGGGGACGGGCGGG	DB &
28564 1375	GGCGCTGGCCCCAACGCCAAGCAGGCCACATACCA	Q D
331		V V
1271 28504	1212 GGCCCCGAGACGACTGTCAACAACACCCCCGAAACGCTGCCTCCCTC	Qy Db
1211 28444		Qу Дъ
1151 28384	1092 GGAGAAACACTCAAGTTCAACGTCTCCAACGGAAAGCCCTTTATCCACGTCATTGACCAG 1	Qy Db
ων	- N3 F	Qу
1031 28264		Фр
71	o − o	Оу
911 28147	852 ATCTACGCACTCCCGTTCCAGATTGCTGTGCGAGACTCCCAGCCGGGTGCGTTCATGACG 9 11111	Qу
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791 28030	732 CTCATCCGCGGCATTCAGAGCACTGGAGTGCAGGCTACGATCAAGCACTTTTTGTGCAAT 7 27971 CTGGTCCGCGGGATCCAGGGCGCACGGCGTGGCCGCCACGCCAAGCACTACGTGGCCAAC 2	Qy Db
731 27970	2 7	ОУ
27910	27851 CGCAAGGGCGTGGACGTCCTCCTCGCCCCGACCCTCAACCTGCACCGCAGCCCGCTGGGC 2	DЬ

1709 28985 1769 29044 1829 29104 1863	CGACGCCCCTCGTCGTCGGCACGGCAAAGGCGTAGACGACCACCTGGCTCGT CTGGAGC-CCCGCCTGGTGGCCGGCCGCACACCGCTCGAGATCCGCGCCACCCGCGAGGAGACCACCGGCAAGCACCGCGAAGCACCGGCAAGCACCGGCAAGCACCGGCAAGCACCGGCAAGCACCGGCAAGCACCCGCAAGCACCGGCAAGCACCGGCAAGCACCTGACGACGACGACCGGCGGCGCTCCTGGGCCTGACGACCTGACGACGACCGAAGCCTCAATCTCGTCCAAGGGCAACACG
1907 29224	CAAGGGCGACACCATCGTCCCGGCCACGG
1955 29284	$\alpha - \alpha$
2015 29344	റ റ
2075 29404	5 CGCGAGCATGAAGCTCCCCGGCGTGCTGGACCAGCTCATTGCCGACGTGGCCGCCGCGAA 1
2135 29464	5 CCCAAACACCGTCGTCGTCATGCAGAACGGGCACCGCGAGGAGATGCCCTGGCTCGACGC
2195 29524	5 CACGCCCGCCGTCATCCAGGCCTGGTACGGCGGCAACGAGAACGGGCAACTCCATTGCCGA
2255 29584	5 CGTCGTCTTTGGCGACTACAACCCCTCGGGCAAGCTGTCCCTCAGCTTGCCCAAGCGCCT
2315 29641	5 GCAGGACAACCCOGCGTTTCTCAACTTCCGCACCGAGGCCGGGGGCGCACGCTGTACGGCGA
2375 29701	5 GGACGTCTACGTCGGGTACAGGTACTACGAGTTTGCCGACAAGGACGTCAATTTCCCCTT
2y 2435 Db 29761	5 TGGCCACGGCCTGTCCTACACCACTTTTGCCTTTTTCCAATCTCTCCGTGTC
Qy 2486 Db 29821	6 TCACAAGGACGGCAAGCTGAGCGTGTCCCTCTCCCGTGAAGAACACCCGGCTCCGTGCCCGG
2y 2546 Db 29881	6 CGCACAGGTGGCCCAGCTCTACGTCAAGCCCCTCCAAGCGGCCCAAGATTAACCGCCCCGT
29 2606 Db 29938	6 CAAGGAGCTCAAGGGCTTCGCAAAGGTCGAACTGCAGCCCGGCGAGACGAGACGAGGCGTGAC
2666 29998	6 AATCGAGGAGCAGGAGAAGTACGTCGCTGCGTATTTTGATGAGGAGC 2712

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REFERENCE
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Best Local Similarity 48.2%;
Matches 1028; Conservative
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CCGTGACGCGGTCGGCGGAGCGCATCGTCAACCAGATGGACAAGTTCGGTCTGCTCCTCG
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                                                                CTGA---
                                                                                             TTGACCAGAGGGCTAGGGAAGTTCTTCAGTTCGTCAAGAAGTGTGCTGCCTCCGGAGTGA 1203
                                                                                                                              C---CCCGGGCACGGACGCCATCACCAAGGGCCTCGACCAGGAGAT----GGGCGTCGAG
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                                                                                                                                                            GCTTCCGAGGAGAAACACTCAAGTTCAACGTCTCCAACGGAAAGCCCTTTATCCACGTCA 1143
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AR173232
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Betlach,M.C. and McDaniel,R.
Bucleic acids encoding narbonolide polyketide
streptomyces narbonensis
Patent: US 6303767-A 11 16-OCT-2001;
Location/Qualifiers
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                                                                -- AGCAGGCCGTCCTGAACGGCACGGTCCCCGAGGCGG
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Pred. No. 5.8e-15;
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                                     GCAAGCTGTCCCTCAGCTTCC-----CCAAGCGCCTGCAGGACAACCCCGCGTTTCTCA
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GCAAGCTCACGCAGAGCTTCCCGGCCGCCGAGAACCAGCACGCCGTCGCCGGCGACCCGA
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Streptomyces narbonensis desc
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                                                                                                                                                                                                                                                             'note="beta glucosidase"
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                                                                                                                                                                                                                                                                                                                                                                                                                       EGGPSGRGLFVGVPA"
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VLMPWLSKTRAVLDMWYPGQAGAEATAALLYGDVNPSGKLTQSFPAAENQHAVAGDPN
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PEAAVTRSAEKIVNQMDKFGLLLATPAPRPERDKAGAQAVSRKVAENGAVLLRNEGQA
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KAVESARKARTAIVFAYDDGTEGVDRPNLSLPGTQDKLISAVADANPNTIVVLNTGSS
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PEKPRSHLAYTGLYLYDNDYVDIAKNIRPSPRGELEITDVNRYYLERGRAELVDLGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(8650. .9684)
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IALPVTAPGTDPVWHLFTVRTDRRDELRDHLDSRGVDTLTHYPVPVHLSPAYAGQAPP
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TGATPVPVEPNEDHPTLDPLLVEKAITPRTRALLPVHLYGHPADLDALRDLADRHGLH
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HTDDHCRGIALVLAGGRAGEVYHIGGGRELTNRELTGILLDSLGADWSSVRRVADRQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="nbmH"
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                                                                                                                                                                                                                                    complement(10840. .12297)
                                                                                                                                                                                                                                                                                         complement(10840.
                                                                                                                                                                                                                                                                                                                            EYGSYLMEIAGREGAP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="NDP-glucose synthase"
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GSTARHLVGLAVRYGNSPETPLEEARHDLGVDRDAFRRLLALFPRVPELRAAVEGGPA
GAYWQNTLLPLERRGVPDSALAGGRVFPYSVGLY PGPTCMFCHECVRVTGARVDPSA
LDTGNAMERSVIDEI PAGNPHALY FSGGLEP LTINPGLGFLAHAAEHGLREPTVYNSF
ALTERTLEROPGLMGHAVRTSLYGLNDEEY EOTTGKKAAFREVWENLKREPOOLAEER
EARINGEAY I VLPGRAHRLLDLVDF 1ADLDESGOGRT IDFVNI REDY SGREDGKLPO
EERAELQEALAAFEERVRERTPGLHIDGY TALBISKAGADAELLEIKRAMMRPTAHPO
VAVQVDLLGDVLLYREAGFPDLDGATRY I AGRNGSKAGADAELLEIKRAMMRPTAHPO
VAVQVDLLGDVLLYREAGFPDLDGATRY I AGRNGSFGTSLTEVVRDY VERGGRVAARDG
DEYFMDGFDQVVTARLNQLERD I ADGWEEARGFLR**

밁 Q δÃ δÃ 밁 В δĀ 망 δÃ 밁 밁 8 В δõ 밁 γQ В δÃ В δÃ 밁 Ş 밁 QV V . р δÃ Db 밁 20 Ş Query Match Best Local Similarity Matches 1028; Conserv 6100 ACGCCGGCAAGAGCATCGCCGTCATCGGCCCGACGGCCGTCGAC-CCCAAGGTCACCGGC 5980 5920 1144 1264 1204 CGGAGAACGGCCCCGAGACGACTGTCAACAACACCCCCGGAAACGGCAGCTCTCCTCCGGA 1263 5880 5767 5707 5647 5470 1084 5590 5410 5820 1024 CATACAGTACCACAGAAGCCGTTGTGGCAGGCCTCGACCTCGAGATGCCCGGACCTCCAC 1083 5530 CGGCCAACAACCAGGAGAACAACCGCTTCAGCGTCAACGCCACGGTCGACGAGCAGACGC 5350 5290 CCCTGGCCAGCACCTTCGACGACTCCATGGCCGACAGCTACGGCAGGGTCATGGGCCGCG 5349 964 904 844 784 724 664 CTCTCGGTGGACGTGGCTTCGAGTCGATTGGTGAGGATCCGTTCCTGGCGGGCTTGGGAG 723 604 544 CGCTCGGTTCCACATTCAACCAAACTCTGCTCGAAGAGGCAGGTAAGATGATGGGCAAAG 603 TCGCCGAGAACGGCGCGGTGCTCCTGCGCAACGAGGGCCAGGCCCTGCCGCTCGCCGGTG CTGCGGCTCTCATCCGCGGCATTCAGAGCACTGGAGTGCAGGCTACGATCAAGCACTTTT AGAAGAAGAAGACGCTGATTGTCGGCCCCAACGCCAAGCCACGCCACATACCACGGCGGAG 1383 CGACTCCGGCGCCCCGCGAGCGTGACAAGGCGGGCGCCCAGGCGGTGTCCCGCAAGG CTGA-----GCTTCCGAGGAGAAACACTCAAGTTCAACGTCTCCAACGGAAAGCCCCTTTATCCACGTCA 1143 C---CCCGGGCACGCACCCATCACCAAGGGCCTCGACCAGGAGAT----GGGCGTCGAG 5819 ACAACGTGCTGCGCACGCAGTGGGGCTTCCAGGGCTGGGTGATGTCCGACTGGCTCGCCA 5766 TCCGTGAAATCTACGCACTCCCGTTCCAGATTGCTGTGCGAGACTCCCAGCCGGGTGCGT 903 CCGTGACGCGGTCGGCGGAGCGCATCGTCAACCAGATGGACAAGTTCGGTCTGCTCCTCG ATGGGATGCTTCGAAAGGAATGGGGTTGGGATGGCCTAATCATGAGCGACTGGTACGGCA 1023 TCATGTGTGCCTATAACGGCGTCAACGGCAAGCCGTCCTGCGGCAACGACGAGCTGCTCA 5706 TCATGACGGCGTACAATGGCATCAATGGCGTGTCGTGCAGCGAGAACCCTAAATATCTTG TGTGCAATGATCAGGAGGACAGGCGCATGATGGTGCAGAGCATCGTCACGGAGCGGGCTC CGGTCGCCCAGATCAAGGGCATCCAGGGTGCGGGTCTGATGACCACGGCCAAGCACTTCG 5529 CACACGGCGGCCGGAACTACGAGACCTTCAGCGAGGACCCCCTGGTCTCCTCGCGCACCG ACGGACGCGCGCTGGGCCAGGACATGGTTCTGGGCCCGATGATGAACAACATCCGGGTGC TCCGCGAGATCGAGTTCCCGGCGTTCGAG---GCGTCCTCGAAGGCCGGCGGCGCCTCCT AGGCCATCGCTAAGAGTGCGCATGTGATCCTCGGCCCGACTATCAACATGCAACGCTCCC 663 Conservative 6.2%; 48.2%; -----AGCAGGCCGTCCTGAACGGCACGGTCCCCGAGGCGG 5919 0; Mismatches 956; Indels 150; Score 184.4; DB 1; Length 17665; Pred. No. 4.9e-15; Gaps 6158 6099 6039 5979 5646 843 5469 783 12;

2571	CCCTCTCCGTGAAGAACACCGGCTCCGTGCCCGGCGCACAGGTGGCCCCAGUTCTACGTCA	Qy 2512	\mathcal{L}
7131	CCTCGTTCACGCAGAGCGCCCCGACCGTGGTGGCACGTCCACGGGGGCGGCCTGAAGGTCA	Db 7072	
2511	CACTTTTGCCTTTTCCAATCTCTCCGTGTCTCACAAGGAC	Qy 2455	0
7071	GUTGGTTCGACAAGGACGTCAAGGACGTCCACTTTGGCCACGGCCTGTCCTACA	Db 7012	
	ACTTCGCACGAGGCGGGCGCACGCTGTACGGCGAGGAGGTCTACGTCGGGTACA	695	0 0
2337 6951	GCAAGCTGTCCCTCAGCTTCCCCAAGCGCCTGCAGGACAACCCCGCGTTTCTCA	689	o o
2283 6891	GGGCAACGAGACGGCAACTCCATTGCCGACGTCGTCTTTGGCGACTACAACCCCTCGG	Qy 2224 Db 6832	D 0
2223 6831	a - a	67	π α
2163 6771		67	Π Ω
2103 6711	ACGCCGACTGGGAGACCGAGGGCGCGAGCCATGAAGCTCCCCGGCGTGCTGG	Qy 204. Db 665.	
2043 6653		6 H	п О
1983 6600	TCCCCGGCCACG	6 L	н о
1923 6540	ACAAGTTCAAGA 	Qy 1864 Db 6505	н о
1863 6504	TCTTCGGCTCCGCCACCGCGAGGAGACGCGCCGCATCAATCTCGTCAAGGGCAACACGT 	6 1	
σ +	2CTCGGCAGCCACA	64	н .
4 9		63 17	
1683 6372 1743	4 TGGTGGACTACTACCACCCCAAGGCGGCAGACACGTGGTACGCCGACATGGAGGGCACGT	Qy 162 Db 631 Qy 168	~ - ~
1623 6312	4 CTGGTACCCCTAACCGCCAGCACTTGACGAGCTCTTCTTCACCAAGACGGACATGCACC		
1563 6278	4 AGCAGTGCCTCACGCCCGACGGCGCTCCGGGCATGCGCTGGAGGGTCTTCAACGAGCCCC	Qy 1504 Db 6219	
6218	* ICHARACHECHAITETACHACHSTEIGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEG	Db 615	

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                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-MAR-1998) P.F. Leadlay, University Of Cambridge, Tennis Court On Mar 25, 1998 this sequence version Overlapping sequences: X60379, M11200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-JUL-1997) P.F. Leadlay, Department Of Biochemistry, University Of Cambridge, Tennis Court Road, Cambridge CB2 1QW, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Analysis of eryBI, eryBIII and eryBVII from the erythromycin biosynthetic gene cluster in Saccharopolyspora erythraea col. Gen. Genet. 258 (1-2), 78-88 (1998)
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Cortes, J. and Leadlay, P.
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Saccharopolyspora erythraea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                  complement(100. .2526)
                                                                                                                                                                                   complement(100. .2526)
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                                                                                                                                                                                                                   /translation="TGGRPGRRGGPGQR"
                                                                                                                                                                                                                                                                  /transl_table=1]
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                  GTGCGCAACACCGGTCAGCGGCGGCGGCAGCGTCGTGCAGGTCTACCTCGGCCCCAGC
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Best Local Similarity
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GTGAAGAACACCGGCTCCGTGCCCGGCGCACAGGTGGCCCAGCTCTACGTCAAGCCCCCTC
                                                                                                                   TTTGCCTTTTCCAATCTCTCCGTGTCTCACAAGGACGGCAAGCTGAGCGTGTCCCTCTCC
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                                                              TTCGAGCGCACCGGGTCGTCGAGCGCACCCGCGACGGCCTCGACGTGACGGTGACCC
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